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# AMMI analysis for stability of chickpea

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## ABSTRACT

Five elite chickpea genotypes along with three check varieties were grown in eight environments during *rabi* 2011-12 season at Pulses Improvement Project, Mahatma Phule Agricultural University, Rahuri to check their stability. The genotypes were grown in randomized block design with three replications. The AMMI analysis of variance for seed yield clearly indicates that the mean sum of square for genotypes is significant, suggesting broad range of diversity among genotypes. The environmental variances are highly significant for all the characters. G x E mean sum of square was significant for seed yield which indicates that the performance of genotypes was differential over the environments. The proportion of sum of square for G x E for seed yield kg/plot was 26.04 %. Three genotypes *viz.,* Phule G-07102, Phule G-09103 and Digvijay exhibited stable performance over all environment (non-interacting)for seed yield kg/plot. The environments E3 (sowing date 1/11/2011), E4 (sowing date 16/11/2011) and E5 (sowing date 1/12/2011) had good conditions for most of the genotypes while at the same time, the PCA score for these three environments were nearly zero indicating all genotypes produced fairly stable seed yield.

**Key words:** Adaptability, AMMI, Chickpea, G x E Interaction, Genotypes.

## INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the third most important food legume. It is grown over 45 countries around the world. Chickpea is the premier pulse crop of Indian subcontinent and India is the largest chickpea producer as well as consumer in the world. It is cultivated in diverse agro-climatic conditions in India and grown under both rainfed and irrigated conditions. Majority of the area is under rainfed farming and is one of the causes of low productivity in the country.

Crop variety developed should show stable performance under different environments, especially in India where wide range of environment is prevailing. Genotypes x environment interaction (GEI) continue to be a challenging issue among plant breeders, geneticists and production agronomist who conduct crop performance trials across diverse environments. GEI can reduce progress for selection.

In the *rabi* track of Maharashtra, the onset of monsoon is often delayed and *kharif* sowing is indefinitely postponed, in that case the farmers used to undertake sowing of chickpea from September to December. This necessitates the testing of stability of newly developed, promising genotypes over the sowing dates.

The major chickpea crop area is grown under rainfed condition in Maharashtra where sowing is carried under residual soil moisture. Under such situation suitable sowing period is last week of September to first week of October for obtaining better yield from rainfed crop. For optimum sown irrigated crop suitable date is 20$^{th}$ October to 10$^{th}$ November. However, some farmers use to sow crop in the month of December or even later. In this situation, it is very important that, the genotype should perform well or it should show stable performance during these sowing periods. Hence, there is enough scope to improve the productivity of this crop by developing stable high yielding varieties suitable for different environments.

The AMMI (Additive Main and Multiplicative Interaction) model suggested by Zobel *et al.*(1988), Gauch(1992) and Purchase (1997) is considered to be a better model for analysis of G x E interaction in yield data of multiloction varietal trials. It not only gives estimate of total G x E interaction effect of each genotype but further partitions it into interaction effects due to individual environments. The present study in chickpea was undertaken to analyze G x E interaction using AMMI model and to evaluate stability and adaptability of genotypes for different sowing dates.

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## MATERIALS AND METHODS

Eight genotypes of chickpea were tested, including three control cultivars (Vijay, Vishal and Digvijay) at eight different environments (sowing dates) during *rabi* 2011-12 season, at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra. Each entry at each environment was sown in randomized block design with three replications at 30 X 10 cm spacing, with net plot size of 4.0 x 1.8 m. The data recorded on seed yield kg/plot for each replication and for each entry at all the environment were utilized for statistical analysis.

The following mathematical model was used for AMMI analysis :

$$Yij=\mu + gi +ej +\Sigma\lambda k +\alpha ik\ yjk +Rij$$

Where, Yij is the the yield of $i^{th}$ genotypes in $j^{th}$ environment; μ the overall mean, gi is the effect of the $i^{th}$ genotype; ej is the effect of the $j^{th}$ enviroment; λk is the square root of the Eigen value of the PCA axis k. Then αik and yjk are the principle components scores for PCA axis k of the $i^{th}$ genotype and $j^{th}$ environment, respectively, and Rij is the residual. The GE interaction sum of squares was subdivided into PCA axis SS, where axis k is regarded as having t + s-1-2k degrees of freedom and t and s are the number of the genotypes and environments; respectively. The data was analyzed by using INDOSTAT statistical package at Mahatma Phule Krishi Vidyapeeth, Rahuri.

## RESULTS AND DISCUSSION

The linear regression model of Eberhart and Russell (1966) is most frequently used for G x E interaction study and in this model a stable genotype should have low deviation from regression ($S^2$di). Therefore, many genotypes having very high potential often get rejected in this model due to high $S^2$di over the range of environments. Thus, a genotype showing high positive interaction at certain environments and negative interaction at others is likely to show high $S^2$di and would be classified as unstable. The Eberhart and Russell model does not provide for critical analysis of interaction of genotypes in specific environments and does not help in identifying promising genotypes which can take advantage of their high positive interaction with the agro-ecological conditions of specific locations or specific agro-management conditions like early or late sowing, high or low fertility, rainfed or irrigated condition *etc*.

AMMI analysis gives estimate of total G x E interaction effect of each genotype and also further partitions it into interaction effects due to individual environments. Low G x E interaction of a genotype indicates stability of the genotype over the range of environments. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and it will be therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environmental condition. Though analysis of G x E interaction of multilocation yield data in AMMI model have been reported by McLaren *et al*. (1998), Ise *et al*. (2001), Vijay kumar *et al*.(2001), Asenjo *et al*.(2003), Mahalingam *et al.*(2006), Naveed *et al.* (2007) and Das *et al.*(2009) in rice, Tarakanovas and Ruzgas (2006) and Mohammadi *et al.* (2007) in wheat, Shinde *et al.* (2002) and Pawar *et al.* (2012) in pearl millet, Hariprasanna *et al.(*2008) in groundnut , Pacheco *et al.* (2005) and in chickpea Rubio *et al.* (2004). All these worker, found significant G x E interaction for grain yield and stressed the usefulness of AMMI analysis for selection of promising genotypes for specific locations or environmental conditions.

The AMMI analysis of variance is presented in Table 1. It clearly indicates that the mean square for genotypes is significant for seed yield kg/plot, suggesting broad range of diversity among genotypes. The environment mean square and G X E mean sum of square were highly significant for seed yield which indicates that the performance of genotypes was different over the environments.

Out of total treatment variation (Trial SS), the proportion of variance due to differences in environment was largest in magnitude for the characters seed yield kg/plot as 50.78% and the proportion of sum of square for G x E was 26.04% for seed yield kg/plot. Thus, ordinary ANOVA model accounted only for the treatment combinations SS attributing to genotypes and environment effects.

**Table 1:** AMMI analysis of variance of characters seed yield kg/ plot of eight gram genotypes tested at eight environments.

| | | Seed yield kg/plot (X10) | | |
|---|---|---|---|---|
| Source | df | SS | MS | % SS |
| Treatment Combination | 63 | 20.948 | 0.333** | 100 |
| Genotype | 7 | 4.858 | 0.123* | 23.19 |
| Environment | 7 | 10.636 | 2.519** | 50.78 |
| GE interaction | 49 | 5.454 | 0.050** | 26.04 |
| PCA I | 13 | 3.836 | 0.064** | 70.33$ |
| PCA II | 11 | 0.552 | 0.050 | 10.13$ |
| PCA III | 9 | 0.439 | 0.049 | 8.05$ |
| PCA IV | 7 | 0.394 | 0.056 | 7.23$ |
| PCA V | 5 | 0.134 | 0.027 | 2.45$ |
| PCA VI | 3 | 0.073 | 0.024 | 1.34$ |
| Residual | 1 | 0.026 | 0.026 | 0.47$ |
| Pooled residual | 49 | 0.627 | 0.039 | |
| Error SS | 62 | 2.136 | 0.034 | |
| Total SS | 191 | 23.084 | 0.121 | |

*,**= Significant at 5% and 1% level of significance, respectively.
$= As per cent of GE interaction SS.

**TABLE 2:** Mean for character seed yield kg/plot of eight genotypes of chickpea grown on eight environment and first PCA scores for the GE interaction effect derived from AMMI model.

| | Environment wise Genotype Mean for seed yield kg/plot | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Genotype** | **$E_1$** (01/10/2011) | **$E_2$** (16/10/2011) | **$E_3$** (01/11/2011) | **$E_4$** (16/11/2011) | **$E_5$** (1/12/2011) | **$E_6$** (16/12/2011) | **$E_7$** (01/01/2012) | **$E_8$** (16/01/2012) | **Overall Genotype Mean** | **FIRST PCA SCORE** |
| Phule G-07102 | 2.510 | 2.547 | 2.533 | 2.633 | 2.297 | 1.517 | 1.637 | 0.750 | 2.053 | 0.344 |
| Phule G-0204-4 | 1.877 | 2.390 | 2.490 | 2.107 | 1.747 | 1.143 | 1.167 | 1.097 | 1.752 | -0.049 |
| Phule G-07101 | 2.553 | 2.407 | 2.323 | 2.253 | 2.003 | 1.013 | 1.303 | 1.007 | 1.858 | 0.491 |
| Phule G-09103 | 2.533 | 2.167 | 2.740 | 2.313 | 1.863 | 1.200 | 1.377 | 0.957 | 1.894 | 0.289 |
| Phule G-06102 | 2.000 | 2.533 | 2.203 | 2.150 | 1.590 | 1.420 | 0.980 | 0.740 | 1.702 | 0.093 |
| Vijay (Check) | 1.867 | 1.880 | 2.320 | 1.927 | 1.843 | 1.370 | 1.223 | 1.183 | 1.702 | -0.391 |
| Vishal (Check) | 1.863 | 1.913 | 2.570 | 2.050 | 1.940 | 1.557 | 1.083 | 0.737 | 1.714 | -0.345 |
| Digvijay (Check) | 2.007 | 2.043 | 2.257 | 2.877 | 2.017 | 1.467 | 1.090 | 1.193 | 1.869 | -0.434 |
| Environmental Mean | 2.151 | 2.235 | 2.430 | 2.289 | 1.912 | 1.336 | 1.232 | 0.958 | | |

The GEI which was significant was further partitioned into PCA axes (IPCA) with per cent contribution to the total GEI variance. All these IPCA axes representing the interaction pattern jointly accounted for interaction component with GEI. These situations seem to arise due to presence of high level of uncontrolled variations but not due to real GEI.

The above analysis, however seems to suggest the presence of a complex, multidirectional variation in genotype-by-environment data. The AMMI model with many IPCA axes are expected to involve rather more noise than the highly complex interaction among genotype and environments. Further, if the AMMI model includes more than one PCA axes, assessment and presentation of genetic stability are not as that of AMMI model (Crossa *et al.*1990). As the first IPCA contributed more in GEI, other IPCA, in present study, were pooled into residual. Thus, AMMI model with first IPCA axis was accepted for further study.

The mean performance IPCA 1 score for both the genotypes and environment used to construct bioplot are represented in Table 2. Bioplot assay presented in Fig. 1 identified three genotypes *viz.*, Phule G – 07102, Phule G-09103 and Digvijay(check) as having general adaptability for seed yield as they were scattered at the right hand side of grand mean level and close to IPCA= 0 line. On the other hand the genotype Phule G-07101 was specifically adapted to favourable environment. Bioplot corresponding to the environment mean and first PCA for seed yield in Fig. 1 clearly indicated that environment, $E_3$ (sowing date 01/11/2011), $E_4$ (sowing date 16/11/2011) and $E_5$ (sowing date 01/12/2011) had good conditions for the most of the genotypes while at the same time, the PCA score for these three environments were nearly zero indicating that all the genotype produced fairly stable seed yield.

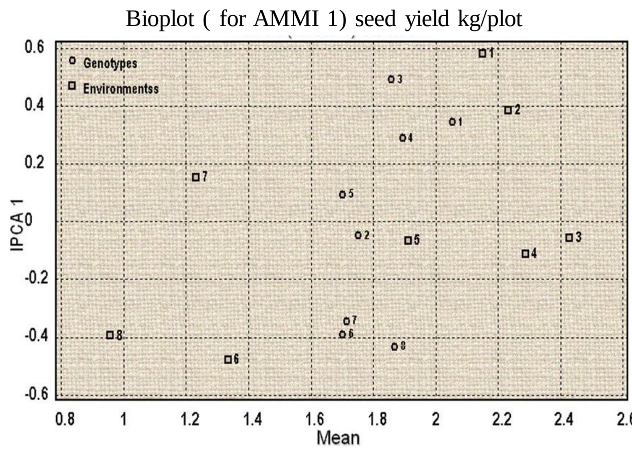


**FIG 1:** Bioplot of AMMI-1 model for a chickpea for seed yield kg/plot with eight genotypes(•) and eight environments (%). The vertical line represents the grand mean of the experiment and horizontal lines IPCA-1.

The environment $E_1$ (sowing date 01/11/2011), had excellent potential for seed yield levels, but were exhibiting high interaction effects and therefore most suitable for specially adapted genotypes. On the other hand environments E 6 (sowing date 16/12/2011), E 7 (sowing date 01/01/2012) and E 8 (sowing date 16/01/2012) had lower seed yield than grand mean and differed for both main effects and interactions, thus performance of genotype in such environments are likely to be quite variable.

AMMI analysis carried out for studying the performance and stability of chickpea genotypes has clearly indicated the usefulness of this model for greater insight into the magnitude and nature of genotype x environment interaction besides identification of genotypes having specific adaptation (interacting) and those which are adaptable (non-interacting). It is also useful for characterizing the environments/ locations broadly suitable for growing a specific or group of the genotypes.

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